Kerr

1633

PAGE: 1

RAW SEQUENCE LISTING
PATENT APPLICATION *US/09/245,198*

DATE: 05/19/2000
TIME: 18:42:50

INPUT SET: S35512.raw *II 10*

┌───┐
│ **This Raw Listing contains the General**   │
│ **Information Section and up to the first 5 pages.** │
└───┘

```
 1                              SEQUENCE LISTING
 2
 3   (1)     General Information:                            ENTERED
 4
 5        (i) APPLICANT: Chicheportiche, Yves
 6                       Browning, Jeffrey L.
 7
 8       (ii) TITLE OF INVENTION: A TUMOR NECROSIS FACTOR RELATED LIGAND
 9
10      (iii) NUMBER OF SEQUENCES: 4
11
12       (iv) CORRESPONDENCE ADDRESS:
13             (A) ADDRESSEE: BIOGEN, INC.
14             (B) STREET: 14 CAMBRIDGE CENTER
15             (C) CITY: CAMBRIDGE
16             (D) STATE: MA
17             (E) COUNTRY: US
18             (F) ZIP: 02142
19
20        (v) COMPUTER READABLE FORM:
21             (A) MEDIUM TYPE: Floppy disk
22             (B) COMPUTER: IBM PC compatible
23             (C) OPERATING SYSTEM: PC-DOS/MS-DOS
24             (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
25
26       (vi) CURRENT APPLICATION DATA:
27             (A) APPLICATION NUMBER:  not yet assigned
28             (B) FILING DATE: 07-May-1997          RECEIVED
29             (C) CLASSIFICATION:
30
31     (viii) ATTORNEY/AGENT INFORMATION:               JUN 08 2000
32             (A) NAME: FLYNN, KERRY A.
33             (B) REGISTRATION NUMBER: 33,693
34             (C) REFERENCE/DOCKET NUMBER: A003 PCT CIP  TECH CENTER 1600/2900
35
36       (ix) TELECOMMUNICATION INFORMATION:
37             (A) TELEPHONE: (617) 679-3583
38             (B) TELEFAX: (617) 679-2838
39
40
41   (2) INFORMATION FOR SEQ ID NO:1:
42
43        (i) SEQUENCE CHARACTERISTICS:
44             (A) LENGTH: 1168 base pairs
45             (B) TYPE: nucleic acid
46             (C) STRANDEDNESS: double
```

--> (line 27 marker)

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47                    (D) TOPOLOGY: linear
48
49          (ii) MOLECULE TYPE: cDNA
50
51         (iii) HYPOTHETICAL: NO
52
53          (iv) ANTI-SENSE: NO
54
55          (vi) ORIGINAL SOURCE:
56                    (A) ORGANISM: TNF family related protein
57
58          (ix) FEATURE:
59                    (A) NAME/KEY: CDS
60                    (B) LOCATION: 2..676
61
62
63          (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
64
65   G GTG CTG AGC CTG GGC CTG GCG CTG GCC TGC CTT GGC CTC CTG CTG            46
66     Val Leu Ser Leu Gly Leu Ala Leu Ala Cys Leu Gly Leu Leu Leu
67      1                   5                  10                  15
68
69   GTC GTG GTC AGC CTG GGG AGC TGG GCA ACG CTG TCT GCC CAG GAG CCT         94
70   Val Val Val Ser Leu Gly Ser Trp Ala Thr Leu Ser Ala Gln Glu Pro
71                       20                  25                  30
72
73   TCT CAG GAG GAG CTG ACA GCA GAG GAC CGC CGG GAG CCC CCT GAA CTG        142
74   Ser Gln Glu Glu Leu Thr Ala Glu Asp Arg Arg Glu Pro Pro Glu Leu
75                   35                  40                  45
76
77   AAT CCC CAG ACA GAG GAA AGC CAG GAT GTG GTA CCT TTC TTG GAA CAA        190
78   Asn Pro Gln Thr Glu Glu Ser Gln Asp Val Val Pro Phe Leu Glu Gln
79               50                  55                  60
80
81   CTA GTC CGG CCT CGA AGA AGT GCT CCT AAA GGC CGG AAG GCG CGG CCT        238
82   Leu Val Arg Pro Arg Arg Ser Ala Pro Lys Gly Arg Lys Ala Arg Pro
83        65                  70                  75
84
85   CGC CGA GCT ATT GCA GCC CAT TAT GAG GTT CAT CCT CGG CCA GGA CAG        286
86   Arg Arg Ala Ile Ala Ala His Tyr Glu Val His Pro Arg Pro Gly Gln
87    80                  85                  90                  95
88
89   GAT GGA GCA CAA GCA GGT GTG GAT GGG ACA GTG AGT GGC TGG GAA GAG        334
90   Asp Gly Ala Gln Ala Gly Val Asp Gly Thr Val Ser Gly Trp Glu Glu
91                       100                 105                 110
92
93   ACC AAA ATC AAC AGC TCC AGC CCT CTG CGC TAC GAC CGC CAG ATT GGG        382
94   Thr Lys Ile Asn Ser Ser Ser Pro Leu Arg Tyr Asp Arg Gln Ile Gly
95                   115                 120                 125
96
97   GAA TTT ACA GTC ATC AGG GCT GGG CTC TAC TAC CTG TAC TGT CAG GTG        430
98   Glu Phe Thr Val Ile Arg Ala Gly Leu Tyr Tyr Leu Tyr Cys Gln Val
99                   130                 135                 140
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100
101    CAC TTT GAT GAG GGA AAG GCT GTC TAC CTG AAG CTG GAC TTG CTG GTG        478
102    His Phe Asp Glu Gly Lys Ala Val Tyr Leu Lys Leu Asp Leu Leu Val
103        145                 150                 155
104
105    AAC GGT GTG CTG GCC CTG CGC TGC CTG GAA GAA TTC TCA GCC ACA GCA        526
106    Asn Gly Val Leu Ala Leu Arg Cys Leu Glu Glu Phe Ser Ala Thr Ala
107    160                 165                 170                 175
108
109    GCA AGC TCT CCT GGG CCC CAG CTC CGT TTG TGC CAG GTG TCT GGG CTG        574
110    Ala Ser Ser Pro Gly Pro Gln Leu Arg Leu Cys Gln Val Ser Gly Leu
111                    180                 185                 190
112
113    TTG CCG CTG CGG CCA GGG TCT TCC CTT CGG ATC CGC ACC CTC CCC TGG        622
114    Leu Pro Leu Arg Pro Gly Ser Ser Leu Arg Ile Arg Thr Leu Pro Trp
115                    195                 200                 205
116
117    GCT CAT CTT AAG GCT GCC CCC TTC CTA ACC TAC TTT GGA CTC TTT CAA        670
118    Ala His Leu Lys Ala Ala Pro Phe Leu Thr Tyr Phe Gly Leu Phe Gln
119            210                 215                 220
120
121    GTT CAC TGAGGGGCCT TGCTCTCCCA GATTCCTTAA ACTTTCCCTG GCTCCAGGAG        726
122    Val His
123        225
124
125    CATCACCACA CCTCCCTACC CCACCCCCAC TCCTCCACCC CCTCGCTGCT CCTTGGTCCA        786
126
127    GTCCTGTCTC TCCTCAAAGG CAGCCAGAGC TTGTTCACAT GTTTCCATTC CACAGACGTA        846
128
129    TCCTTGCTCT TCTTAACATC CCATCCCACC ACAACTATCC ACCTCACTAG CTCCCAAAGC        906
130
131    CCCTACTTAT CCCTGACTCC CCCACCCACT CACCCGACCA CGTGTTTATT GACTTTGTGC        966
132
133    ACCAGGCACT GAGATGGGCT GGACCTGGTG GCAGGAAGCC AGAGAACCTG GGACTAGGCC       1026
134
135    AGAAGTTCCC AACTGTGAGG GGGAAGAGCT GGGGACAAGC TCCTCCCTGG ATCCCTGTGG       1086
136
137    ATTTTGAAAA GATACTATTT TTATTATTAT TGTGACAAAA TGTTAAATGG ATATTAAAGA       1146
138
139    GAATAAATCA TGATTTCTCT TC                                               1168
140
141
142    (2) INFORMATION FOR SEQ ID NO:2:
143
144            (i) SEQUENCE CHARACTERISTICS:
145                    (A) LENGTH: 225 amino acids
146                    (B) TYPE: amino acid
147                    (D) TOPOLOGY: linear
148
149            (ii) MOLECULE TYPE: protein
150
151            (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:
152
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153   Val Leu Ser Leu Gly Leu Ala Leu Ala Cys Leu Gly Leu Leu Leu Val
154    1               5                  10                  15

155

156   Val Val Ser Leu Gly Ser Trp Ala Thr Leu Ser Ala Gln Glu Pro Ser
157            20                  25                  30

158

159   Gln Glu Glu Leu Thr Ala Glu Asp Arg Arg Glu Pro Pro Glu Leu Asn
160            35                  40                  45

161

162   Pro Gln Thr Glu Glu Ser Gln Asp Val Val Pro Phe Leu Glu Gln Leu
163        50                  55                  60

164

165   Val Arg Pro Arg Arg Ser Ala Pro Lys Gly Arg Lys Ala Arg Pro Arg
166    65              70                  75                  80

167

168   Arg Ala Ile Ala Ala His Tyr Glu Val His Pro Arg Pro Gly Gln Asp
169                85                  90                  95

170

171   Gly Ala Gln Ala Gly Val Asp Gly Thr Val Ser Gly Trp Glu Glu Thr
172            100                 105                 110

173

174   Lys Ile Asn Ser Ser Ser Pro Leu Arg Tyr Asp Arg Gln Ile Gly Glu
175            115                 120                 125

176

177   Phe Thr Val Ile Arg Ala Gly Leu Tyr Tyr Leu Tyr Cys Gln Val His
178        130                 135                 140

179

180   Phe Asp Glu Gly Lys Ala Val Tyr Leu Lys Leu Asp Leu Leu Val Asn
181    145                 150                 155                 160

182

183   Gly Val Leu Ala Leu Arg Cys Leu Glu Glu Phe Ser Ala Thr Ala Ala
184                165                 170                 175

185

186   Ser Ser Pro Gly Pro Gln Leu Arg Leu Cys Gln Val Ser Gly Leu Leu
187            180                 185                 190

188

189   Pro Leu Arg Pro Gly Ser Ser Leu Arg Ile Arg Thr Leu Pro Trp Ala
190        195                 200                 205

191

192   His Leu Lys Ala Ala Pro Phe Leu Thr Tyr Phe Gly Leu Phe Gln Val
193        210                 215                 220

194

195   His
196   225
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198   (2) INFORMATION FOR SEQ ID NO:3:

199

200       (i) SEQUENCE CHARACTERISTICS:
201           (A) LENGTH: 1373 base pairs
202           (B) TYPE: nucleic acid
203           (C) STRANDEDNESS: double
204           (D) TOPOLOGY: linear
205
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RAW SEQUENCE LISTING
PATENT APPLICATION US/09/245,198

DATE: 05/19/2000
TIME: 18:42:51

INPUT SET: S35512.raw

```
206        (ii) MOLECULE TYPE: cDNA
207
208      (iii) HYPOTHETICAL: NO
209
210       (iv) ANTI-SENSE: NO
211
212       (vi) ORIGINAL SOURCE:
213             (A) ORGANISM: TNF family related protein
214
215       (ix) FEATURE:
216             (A) NAME/KEY: CDS
217             (B) LOCATION: 1..852
218
219
220       (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:
221
222    ATG TCA TTG TTA GAC TTT GAA ATT TCC GCC CGC CGG CTC CCC CTC CCC        48
223    Met Ser Leu Leu Asp Phe Glu Ile Ser Ala Arg Arg Leu Pro Leu Pro
224     1               5                  10                  15
225
226    CGA TCC CTC GGG TCC CGG GAT GGG GGG GCG GTG AGG CAG GCA CAG CCC        96
227    Arg Ser Leu Gly Ser Arg Asp Gly Gly Ala Val Arg Gln Ala Gln Pro
228             20                  25                  30
229
230    CCC GCC CCC ATG GCC GCC CGT CGG AGC CAG AGG CGG AGG GGG CGC CGG       144
231    Pro Ala Pro Met Ala Ala Arg Arg Ser Gln Arg Arg Arg Gly Arg Arg
232             35                  40                  45
233
234    GGG GAG CCG GGC ACC GCC CTG CTG GTC CCG CTC GCG CTG GGC CTG GGC       192
235    Gly Glu Pro Gly Thr Ala Leu Leu Val Pro Leu Ala Leu Gly Leu Gly
236         50                  55                  60
237
238    CTG GCG CTG GCC TGC CTC GGC CTC CTG CTG GCC GTG GTC AGT TTG GGG       240
239    Leu Ala Leu Ala Cys Leu Gly Leu Leu Leu Ala Val Val Ser Leu Gly
240     65                  70                  75                  80
241
242    AGC CGG GCA TCG CTG TCC GCC CAG GAG CCT GCC CAG GAG GAG CTG GTG       288
243    Ser Arg Ala Ser Leu Ser Ala Gln Glu Pro Ala Gln Glu Glu Leu Val
244                 85                  90                  95
245
246    GCA GAG GAG GAC CAG GAC CCG TCG GAA CTG AAT CCC CAG ACA GAA GAA       336
247    Ala Glu Glu Asp Gln Asp Pro Ser Glu Leu Asn Pro Gln Thr Glu Glu
248             100                 105                 110
249
250    AGC CAG GAT CCT GCG CCT TTC CTG AAC CGA CTA GTT CGG CCT CGC AGA       384
251    Ser Gln Asp Pro Ala Pro Phe Leu Asn Arg Leu Val Arg Pro Arg Arg
252         115                 120                 125
253
254    AGT GCA CCT AAA GGC CGG AAA ACA CGG GCT CGA AGA GCG ATC GCA GCC       432
255    Ser Ala Pro Lys Gly Arg Lys Thr Arg Ala Arg Arg Ala Ile Ala Ala
256         130                 135                 140
257
258    CAT TAT GAA GTT CAT CCA CGA CCT GGA CAG GAC GGA GCG CAG GCA GGT       480
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SEQUENCE VERIFICATION REPORT
PATENT APPLICATION   *US/09/245,198*

DATE: 05/19/2000
TIME: 18:42:51

INPUT SET: S35512.raw

Line	Error	Original Text
27	Wrong application Serial Number	(A) APPLICATION NUMBER: not yet assigned